

SEQUENCE LISTING

78-0B10 amino acid sequence (SEQ ID NO:1)

5	Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu	1	5	10	15
	Ala Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr	20	25	30	
	Ala Asp Ile Ser Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu	35	40	45	
10	Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu	50	55	60	
	Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys	65	70	75	80
	Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr	85	90	95	
15	Leu Gly Ile Ile Ala Ala Pro Val Ser Asp Lys Tyr Ile Glu Arg Glu	100	105	110	
	Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Ile Phe Cys Ser	115	120	125	
20	Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser	130	135	140	
	Val Glu Thr Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr	145	150	155	160
	Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp	165	170	175	
25	Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala	180	185	190	
	Leu Val Met Phe Ser Ser Gly Thr Thr Gly Val Pro Lys Gly Val Met	195	200	205	
30	Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Leu Ala Lys Asp Pro	210	215	220	
	Thr Phe Gly Asn Ala Ile Asn Pro Thr Thr Ala Ile Leu Thr Val Ile	225	230	235	240
	Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr	245	250	255	
35	Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe	260	265	270	
	Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro	275	280	285	
40	Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp	290	295	300	
	Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys	305	310	315	320
	Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg	325	330	335	
45					

Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro
 340 345 350
 Lys Gly Asp Ala Arg Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His
 355 360 365
 5 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn
 370 375 380
 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Ala Met Ile Met Lys Gly Tyr
 385 390 395 400
 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp
 10 405 410 415
 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr
 420 425 430
 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val
 435 440 445
 15 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
 450 455 460
 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro
 465 470 475 480
 Ala Ala Gly Val Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile
 20 485 490 495
 Val Gln Asp Phe Val Ser Ser Gln Val Ser Thr Ala Lys Trp Leu Arg
 500 505 510
 Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys
 515 520 525
 25 Ile Asp Arg Lys Val Leu Arg Gln Met Phe Glu Lys His Thr Asn Gly
 530 535 540

90-1B5 amino acid sequence (SEQ ID NO:2)

30 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu
 1 5 10 15
 Glu Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr
 20 25 30
 35 Ala Asp Ile Pro Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu
 35 40 45
 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu
 50 55 60
 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys
 40 65 70 75 80
 Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr
 85 90 95
 Leu Gly Ile Ile Val Ala Pro Val Asn Asp Lys Tyr Ile Glu Arg Glu
 100 105 110
 45 Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Val Phe Cys Ser
 115 120 125
 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser

	130	135	140	
	Ile	Glu	Thr	Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr
	145	150	155	160
5	Gln	Cys	Leu	Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp
	165	170	175	
	Val	Lys	Lys	Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala
	180	185	190	
	Leu	Ile	Met	Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
	195	200	205	
10	Leu	Thr	His	Lys Asn Ile Val Ala Arg Phe Ser Leu Ala Lys Asp Pro
	210	215	220	
	Thr	Phe	Gly	Asn Ala Ile Asn Pro Thr Thr Ala Ile Leu Thr Val Ile
	225	230	235	240
	Pro	Phe	His	His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr
15	245	250	255	
	Cys	Gly	Phe	Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe
	260	265	270	
	Leu	Gln	Ser	Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro
	275	280	285	
20	Thr	Leu	Met	Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp
	290	295	300	
	Leu	Ser	His	Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys
	305	310	315	320
	Glu	Ile	Gly	Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg
25	325	330	335	
	Gln	Gly	Tyr	Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro
	340	345	350	
	Lys	Gly	Asp	Ala Lys Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His
	355	360	365	
30	Ala	Val	Lys	Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn
	370	375	380	
	Glu	Pro	Gly	Glu Leu Tyr Phe Lys Gly Pro Met Ile Met Lys Gly Tyr
	385	390	395	400
	Tyr	Asn	Asn	Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp
35	405	410	415	
	Leu	Arg	Ser	Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr
	420	425	430	
	Ile	Val	Asp	Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val
	435	440	445	
40	Ala	Pro	Ala	Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
	450	455	460	
	Asp	Ala	Gly	Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro
	465	470	475	480
	Ala	Ala	Gly	Val Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile
45	485	490	495	
	Val	Gln	Asp	Tyr Val Ala Ser Gln Val Ser Thr Ala Lys Trp Leu Arg
	500	505	510	

Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys
515 520 525
Ile Asp Arg Lys Val Leu Arg Gln Met Phe Glu Lys His Thr Asn Gly
530 535 540

5

133-1B2 amino acid sequence (SEQ ID NO:3)

10 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu
1 5 10 15
Glu Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr
20 25 30
Ala Asp Ile Pro Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu
35 40 45
15 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu
50 55 60
Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys
65 70 75 80
Ser Glu Asn Ser Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr
85 90 95
20 Leu Gly Ile Ile Val Ala Pro Val Asn Asp Lys Tyr Ile Glu Arg Glu
100 105 110
Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Val Phe Cys Ser
115 120 125
25 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser
130 135 140
Ile Glu Thr Ile Ile Ile Leu Asp Leu Asn Asp Asp Leu Gly Gly Tyr
145 150 155 160
Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp
165 170 175
30 Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala
180 185 190
Leu Ile Met Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
195 200 205
35 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Ile Ala Lys Asp Pro
210 215 220
Thr Phe Gly Asn Ala Ile Asn Pro Thr Ser Ala Ile Leu Thr Val Ile
225 230 235 240
Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr
245 250 255
40 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe
260 265 270
Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro
275 280 285
45 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp
290 295 300
Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys

Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Val Phe Cys Ser
 115 120 125
 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser
 130 135 140
 5 Ile Glu Thr Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr
 145 150 155 160
 Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp
 165 170 175
 Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala
 180 185 190
 10 Ser Ile Met Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
 195 200 205
 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Ile Ala Lys Asp Pro
 210 215 220
 15 Thr Phe Gly Asn Ala Ile Asn Pro Thr Ser Ala Ile Leu Thr Val Ile
 225 230 235 240
 Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr
 245 250 255
 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe
 260 265 270
 20 Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro
 275 280 285
 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp
 290 295 300
 25 Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys
 305 310 315 320
 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg
 325 330 335
 Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro
 340 345 350
 30 Lys Gly Asp Ala Lys Pro Gly Ser Thr Gly Lys Ile Val Pro Leu His
 355 360 365
 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn
 370 375 380
 35 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Pro Met Ile Met Lys Gly Tyr
 385 390 395 400
 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp
 405 410 415
 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr
 420 425 430
 40 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val
 435 440 445
 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
 450 455 460
 45 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro
 465 470 475 480
 Ala Ala Gly Val Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile

	485	490	495	
	Val Gln Asp Tyr Val Ala Ser Gln Val Ser Thr Ala Lys Trp Leu Arg			
	500	505	510	
5	Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys			
	515	520	525	
	Ile Asp Arg Lys Val Leu Arg Gln Met Leu Glu Lys His Thr Asn Gly			
	530	535	540	

78-0B10 (SEQ ID NO:5)

10 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCT
TGGCTGATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGC
AGATATTTCCGGATGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTT
TTATATGAAGAGTTTTTAAAATTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAA
GTATGGATTAAAACAAAACGACACAATAGCGGTGTGTAGCGAAAATGGTTTG
15 CAATTTTTCCTTCTGTAATTGCATCATTGTATCTTGGAATAATTGCAGCACCT
GTTAGTGATAAATACATTGAACGTGAATTAATACACAGTCTTGGTATTGTAAA
ACCACGCATAATTTTTTGCTCCAAGAATACTTTTCAAAAAGTACTGAATGTAA
AATCTAAATTAATAATCTGTAGAACTATTATTATATTAGACTTAAATGAAGAC
TTAGGAGGTTATCAATGCCTCAACAACTTTATTTCTCAAAATTCCGATAGTAA
20 TCTGGACGTAAAAAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTG
CGTTGGTAATGTTTTCTTCTGGTACAACCTGGTGTTCGGAAGGGAGTCATGCTA
ACTCACAAGAATATTGTTGCACGATTTTCTCTTGCAAAAAGATCCTACTTTTGG
TAACGCAATTAATCCCACGACAGCAATTTTAACGGTAATACCTTTCCACCATG
GTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGGATTCCGAGTTGTT
25 CTAATGCACACGTTTGAAGAAAACTATTTCTACAATCATTACAAGATTATAA
AGTGGAAGTACTTTACTTGTACCAACATTAATGGCATTTCCTTGCAAAAAGTG
CATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTGG
CGCACCTTTATCAAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTA
AACTTTGTCAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTAAT
30 TACACCGAAAGGTGACGCCAGACCGGGATCAACTGGTAAAATAGTACCATT
CACGCTGTAAAGTTGTGATCCTACAACAGGAAAAATTTTGGGGCCAAATG
AACCTGGAGAATTGTATTTTAAAGGCGCCATGATAATGAAGGGTTATTATAA
TAATGAAGAAGCTACTAAAGCAATTATTGATAATGACGGATGGTTGCGCTCT
GGTGATATTGCTTATTATGACAATGATGGCCATTTTTATATTGTGGACAGGCT
35 GAAGTCATTAATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAG
GGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATACC
GGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGA
AAATATCTAAACGAACAAATCGTACAAGATTTTGTTCAGTCAAGTTTCAAC
AGCCAAATGGCTACGTGGTGGGGTGAAATTTTGGATGAAATTCCCAAAGGA
40 TCAACTGGAAAAATTGACAGAAAAGTGTTAAGACAAATGTTTGAAAAACACA
CCAATGGG

90-1B5 (SEQ ID NO:6)

45 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCC
CTTGGAAGA 60
TGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGATA
TTCCGGGCTG 120

CATAGCATTGACAAATGCTCATACAAAAGAAAATGTTTTATATGAAGAGT
TTCTGAAACT 180
GTCGTGTCGTTTAGCGGAAAGTTTTAAAAAGTATGGATTAAAACAAAACG
ACACAATAGC 240
5 GGTGTGTAGCGAAAATGGTCTGCAATTTTTCCTTCCTGTAATTGCATCATT
GTATCTTGG 300
AATAATTGTGGCACCTGTTAACGATAAATACATTGAACGTGAATTAATAC
ACAGTCTTGG 360
TATTGTAAAACCACGCATAGTTTTTTTGCTCCAAGAATACTTTTCAAAAAGT
10 ACTGAATGT 420
AAAATCTAAATTAAAATCTATTGAACTATTATTATATTAGACTTAAATGA
AGACTTAGG 480
AGGTTATCAATGCCTCAACAACCTTTATTTCTCAAAATTCCGATAGTAATCT
GGACGTA 540
15 AAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGATTAT
GTTTTCTTC 600
TGGTACAACCTGGTCTGCCGAAGGGAGTCATGCTAACTCACAAGAATATTG
TTGCACGATT 660
TTCTCTTGCAAAAGATCCTACTTTTGGTAACGCAATTAATCCCACGACAGC
20 AATTTTAAC 720
GGTAATACCTTTCCACCATGGTTTTGGTATGATGACCACATTAGGATACTT
TACTTGTGG 780
ATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAAACTATTTCTACAATC
ATTACAAGA 840
25 TTATAAAGTGGAAGTACTTTACTTGTACCAACATTAATGGCATTCTTTCG
AAAAAGTGC 900
ATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTG
GCGCACCTT 960
ATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTAACTTTG
30 TCAGGCAAGG 1020
GTATGGATTAACAGAAACCACTTCGGCTGTTTTAATTACACCGAAAGGTG
ACGCCAAACC 1080
GGGATCAACTGGTAAAATAGTACCATTTACGCTGTAAAGTTGTCGATCC
TACAACAGG 1140
35 AAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTTAAAGGCCCGA
TGATAATGAA 1200
GGGTTATTATAATAATGAAGAAGCTACTAAAGCAATTATTGATAATGACG
GATGGTTGCG 1260
CTCTGGTGATATTGCTTATTATGACAATGATGGCCATTTTATATTGTGGA
40 CAGGCTGAA 1320
GTCAGTATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAGG
GAATACTCTT 1380
ACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATACCGGATGAAG
CCGCGGGCGA 1440
45 GCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAAAATATCTAAACGAAC
AAATCGTACA 1500

AGATTATGTTGCCAGTCAAGTTTCAACAGCCAAATGGCTACGTGGTGGGG
TGAAATTTTT 1560
GGATGAAATTCCCAAAGGATCAACTGGAAAAATTGACAGAAAAGTGTTA
AGACAAATGTT 1620
5 TGAAAAACACACCAATGGG 1639

133-1B2 (SEQ ID NO:7)

AGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCT
TGGAAGATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGC
10 AGATATTCCGGGCTGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTT
TTATATGAAGAGTTTCTGAAACTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAA
GTATGGATTAAAACAAAACGACACAATAGCGGTGTGTAGCGAAAATAGTCTG
CAATTTTTCCTTCCTGTAATTGCATCATTGTATCTTGGAATAATTGTGGCACCT
GTTAACGATAAATACATTGAACGTGAATTAATACACAGTCTTGGTATTGTAA
15 AACCACGCATAGTTTTTGTCTCCAAGAATACTTTTCAAAAAGTACTGAATGTA
AAATCTAAATTAATAATCTATTGAACTATTATTATATTAGACTTAAATGATGA
CTTAGGAGGTTATCAATGCCTCAACAACCTTTATTTCTCAAAATTCCGATAGTA
ATCTGGACGTAAAAAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTT
GCGTTGATTATGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCT
20 AACTCACAAGAATATTGTTGCACGATTTTCTATTGCAAAAGATCCTACTTTTG
GTAACGCAATTAATCCACGTCAGCAATTTTAACGGTAATACCTTTCCACCAT
GGTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGGATTCCGAGTTGT
TCTAATGCACACGTTTGAAGAAAAACTATTTCTACAATCATTACAAGATTATA
AAGTGGAAAGTACTTTACTTGTACCAACATTAATGGCATTCTTGCAAAAAGT
25 GCATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTG
GCGCACCTTTATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATT
AACTTTGTGTCAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTA
ATTACACCGAAAGGTGACGCCAAACCGGGATCAACTGGTAAAATAGTACCAT
TTCACGCTGTAAAGTTGTGCGATCCTACAACAGGAAAAATTTTGGGGCCAAA
30 TGAACCTGGAGAATTGTATTTTAAAGGCCCGATGATAATGAAGGGTTATTAT
AATAATGAAGAAGCTACTAAAGCAATTATTGATAATGACGGATGGTTGCGCT
CTGGTGATATTGCTTATTATGACAATGATGGCCATTTTATATTGTGGACAGG
CTGAAGTCACTGATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTG
AGGGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATA
35 CCGGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTG
GAAAATATCTAAACGAACAAATCGTACAAGATTATGTTGCCAGTCAAGTTTC
AACAGCCAAATGGCTACGTGGTGGGGTGATATTTTGGATGAAATTCCCAA
GGATCAACTGGAAAAATTGACAGAAAAGTGTTAAGACAAATGTTAGAAAAA
CACACCAATGGG

146-1H2 (SEQ ID NO:8)

GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCT
TGGAAGATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGC
AGCTATTCCGGGCTGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTT
45 TTATATGAAGAGTTTCTGAAACTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAA
GTATGGATTAAAACAAAACGACACAATAGCGGTGTGTAGCGAAAATAGTCTG
CAATTTTTCCTTCCTGTAATTGCATCATTGTATCTTGGAATAATTGTGGCACCT

5 GTTAACGATAAATACATTGAACGTGAATTAATACACAGTCTTGGTATTGTAA
AACCACGCATAGTTTTTTGCTCCAAGAATACTTTTCAAAAAGTACTGAATGTA
AAATCTAAATTAATAATCTATTGAACTATTATTATATTAGACTTAAATGAAGA
CTTAGGAGGTTATCAATGCCTCAACAACCTTTATTTCTCAAAATTCCGATAGTA
ATCTGGACGTAAAAAAATTTAAACCCTATTCTTTTAATCGAGACGATCAGGTT
10 GCGTCGATTATGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCT
AACTCACAAGAATATTGTTGCACGATTTTCTATTGCAAAAAGATCCTACTTTTG
GTAACGCAATTAATCCCACGTCAGCAATTTTAACGGTAATACCTTTCCACCAT
GGTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGGATTCCGAGTTgTT
CTAATGCACACGTTTGAAGAAAACTATTTCTACAATCATTACAAGATTATAA
AGTGGAAGTACTTTACTTGTACCAACATTAATGGCATTTCCTTGCAAAAAGTG
CATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTGG
CGCACCTTTATCAAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTA
15 AACTTTGTCAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTAAT
TACACCGAAAGGTGACGCCAAACCGGGATCAACTGGTAAAATAGTACCATTA
CACGCTGTAAAGTTGTCTGATCCTACAACAGGAAAAATTTTGGGGCCAAATG
AACCTGGAGAATTGTATTTTAAAGGCCCGATGATAATGAAGGGTTATTATAA
TAATGAAGAAGCTACTAAAGCAATTATTGATAATGACGGATGGTTGCGCTCT
20 GGTGATATTGCTTATTATGACAATGATGGCCATTTTTATATTGTGGACAGGCT
GAAGTCACTGATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAG
GGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATACC
GGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGA
AAATATCTAAACGAACAAATCGTACAAGATTATGTTGCCAGTCAAGTTTCAA
CAGCCAAATGGCTACGTGGTGGGGTGAAATTTTTGGATGAAATCCCAAAGG
25 ATCAACTGGAAAAATTGACAGAAAAGTGTTAAGACAAATGTTAGAAAAACA
CACCAATGGG